

SEQUENCE LISTING

(1) General Information

- (i) APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.
- (ii) TITLE OF INVENTION: Novel Polypeptide Having Water Channel Activity and DNA sequence
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.
 - (B) STREET: 9 ? 19 Shimoshinjo 3-chome Higashiyodogawa-Ku
 - (C) CITY: Osaka
 - (D) STATE: Osaka
 - (E) COUNTRY: JAPAN
 - (F) ZIP: 533-0021
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage
 - (B) COMPUTER: IBM PS/2 or compatibles
 - (C) OPERATING SYSTEM: WINDOWS 95/97
 - (D) SOFTWARE: Microsoft Word 97
- (vi) CURRENT APPLICATION DATE:
 - (A) APPLICATION NUMBER: 09/381,810
 - (B) FILING DATE: 19-OCT-1999
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATE
 - (A) APPLICATION NUMBER: JP09 094845
 - (B) FILING DATE: 28-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Burton A. Amernick
 - (B) REGISTRATION NUMBER: 24852
 - (C) REFERENCE/DOCKET NUMBER: 1581/00156
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)331-7111
 - (B) FAX: (202)293-6229

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH F342 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY F linear
- (ii) MORECULE TYPE F peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met
5 10 15
Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys
20 25 30
Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met
35 40 45
Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr
50 55 60
Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met
65 70 75 80
Gly Val His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala
85 90 95
Val Thr Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe

100	105	110
Pro Val Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala		
115	120	125
Thr Ile Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly		
130	135	140
Gln Leu Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr		
145	150	155
Tyr Leu Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala		
165	170	175
Trp Leu Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln		
180	185	190
Glu Asn Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile		
195	200	205
Leu Val Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala		
210	215	220
Ile Asn Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala		
225	230	235
Gly Trp Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val		
245	250	255
Pro Val Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr		
260	265	270
Leu Val Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu		
275	280	285
Asp Ser Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met		
290	295	300
Gly Ser His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser		
305	310	315
Pro Ala Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser		
325	330	335
Met Ala Leu Glu His Phe		
340		

(2) INFORMATION FOR SEQ ID No F2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH F1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY F linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) TISSUE TYPE: fat tissue

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION F173..1198
- (C) IDENTIFICATION METHOD: by experiment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGCTCTGGAC TGGGGACACA GGGATAGCTG AGCCCCAGCT GGGGGTGGAA GCTGAGCCAG	60
GGACAGTCAC GGAGGAACAA GATCAAGATG CGCTGTAACT GAGAAGCCCC CAAGGCGGAG	120
GCTGAGAACATC AGAGACATT CAGCAGACAT CTACAAATCT GAAAGACAAA AC ATG GTT	178
	Met Val
	1
CAA GCA TCC GGG CAC AGG CGG TCC ACC CGT GGC TCC AAA ATG GTC TCC	226
Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met Val Ser	

TGG	TCC	GTG	ATA	GCA	AAG	ATC	CAG	GAA	ATA	CTG	CAG	AGG	AAG	ATG	GTG		274
Trp	Ser	Val	Ile	Ala	Lys	Ile	Gln	Glu	Ile	Leu	Gln	Arg	Lys	Met	Val		
20						25					30						
CGA	GAG	TTC	CTG	GCC	GAG	TTC	ATG	AGC	ACA	TAT	GTC	ATG	ATG	GTA	TTC		322
Arg	Glu	Phe	Leu	Ala	Glu	Phe	Met	Ser	Thr	Tyr	Val	Met	Met	Val	Phe		
35						40				45			50				
GGC	CTT	GGT	TCC	GTG	GCC	CAT	ATG	GTT	CTA	AAT	AAA	AAA	TAT	GGG	AGC		370
Gly	Leu	Gly	Ser	Val	Ala	His	Met	Val	Leu	Asn	Lys	Lys	Tyr	Gly	Ser		
						55			60			65					
TAC	CTT	GGT	GTC	AAC	TTG	GGT	TTT	GGC	TTC	GGA	GTC	ACC	ATG	GGA	GTG		418
Tyr	Leu	Gly	Val	Asn	Leu	Gly	Phe	Gly	Phe	Gly	Val	Thr	Met	Gly	Val		
						70			75			80					
CAC	GTG	GCA	GGC	CGC	ATC	TCT	GGA	GCC	CAC	ATG	AAC	GCA	GCT	GTG	ACC		466
His	Val	Ala	Gly	Arg	Ile	Ser	Gly	Ala	His	Met	Asn	Ala	Ala	Val	Thr		
						85			90			95					
TTT	GCT	AAC	TGT	GCG	CTG	GGC	CGC	GTG	CCC	TGG	AGG	AAG	TTT	CCG	GTC		514
Phe	Ala	Asn	Cys	Ala	Leu	Gly	Arg	Val	Pro	Trp	Arg	Lys	Phe	Pro	Val		
						100			105			110					
TAT	GTG	CTG	GGG	CAG	TTC	CTG	GGC	TCC	TTC	CTG	GCG	GCT	GCC	ACC	ATC		562
Tyr	Val	Leu	Gly	Gln	Phe	Leu	Gly	Ser	Phe	Leu	Ala	Ala	Ala	Thr	Ile		
						115			120			125			130		
TAC	AGT	CTC	TTC	TAC	ACG	GCC	ATT	CTC	CAC	TTT	TCG	GGT	GGA	CAG	CTG		610
Tyr	Ser	Leu	Phe	Tyr	Thr	Ala	Ile	Leu	His	Phe	Ser	Gly	Gly	Gln	Leu		
						135			140			145					
ATG	GTG	ACC	GGT	CCC	GTC	GCT	ACA	GCT	GGC	ATT	TTT	GCC	ACC	TAC	CTT		658
Met	Val	Thr	Gly	Pro	Val	Ala	Thr	Ala	Gly	Ile	Phe	Ala	Thr	Tyr	Leu		
						150			155			160					
CCT	GAT	CAC	ATG	ACA	TTG	TGG	CGG	GGC	TTC	CTG	AAT	GAG	GCG	TGG	CTG		706
Pro	Asp	His	Met	Thr	Leu	Trp	Arg	Gly	Phe	Leu	Asn	Glu	Ala	Trp	Leu		
						165			170			175					
ACC	GGG	ATG	CTC	CAG	CTG	TGT	CTC	TTC	GCC	ATC	ACG	GAC	CAG	GAG	AAC		754
Thr	Gly	Met	Leu	Gln	Leu	Cys	Leu	Phe	Ala	Thr	Thr	Asp	Gln	Glu	Asn		
						180			185			190					
AAC	CCA	GCA	CTG	CCA	GGA	ACA	GAG	GCG	CTG	GTG	ATA	GGC	ATC	CTC	GTG		802
Asn	Pro	Ala	Leu	Pro	Gly	Thr	Glu	Ala	Leu	Ile	Gly	Ile	Leu	Val			
						195			200			205			210		
GTC	ATC	ATC	GGG	GTG	TCC	CTT	GGC	ATG	AAC	ACA	GGA	TAT	GCC	ATC	AAC		850
Val	Ile	Ile	Gly	Val	Ser	Leu	Gly	Met	Asn	Thr	Gly	Tyr	Ala	Ile	Asn		
						215			220			225					
CCG	TCC	CGG	GAC	CTG	CCC	CCC	CGC	ATC	TTC	ACC	TTC	ATT	GCT	GGT	TGG		898
Pro	Ser	Arg	Asp	Leu	Pro	Pro	Arg	Ile	Phe	Thr	Phe	Ile	Ala	Gly	Trp		
						230			235			240					
GCG	AAA	CAG	GTC	TTC	AGC	AAT	GGG	GAG	AAC	TGG	TGG	TGG	GTG	CCA	GTG		946
Gly	Lys	Gln	Val	Phe	Ser	Asn	Gly	Glu	Asn	Trp	Trp	Trp	Val	Pro	Val		
						245			250			255					
GTG	GCA	CCA	CTT	CTG	GGT	GCC	TAT	CTA	GGT	GGC	ATC	ATC	TAC	CTG	GTC		994
Val	Ala	Pro	Leu	Leu	Gly	Ala	Tyr	Leu	Gly	Gly	Ile	Ile	Tyr	Leu	Val		
						260			265			270					
TTC	ATT	GGC	TCC	ACC	ATC	CCA	CGG	GAG	CCC	CTG	AAA	TTG	GAG	GAT	TCT		1042
Phe	Ile	Gly	Ser	Thr	Ile	Pro	Arg	Glu	Pro	Leu	Lys	Leu	Glu	Asp	Ser		
						275			280			285			290		
GTG	GCG	TAT	GAA	GAC	CAC	GGG	ATA	ACC	GTA	TTG	CCC	AAG	ATG	GGA	TCT		1090
Val	Ala	Tyr	Glu	Asp	His	Gly	Ile	Thr	Val	Leu	Pro	Lys	Met	Gly	Ser		
						295			300			305					
CAT	GAA	CCC	ACG	ATC	TCT	CCC	CTC	ACC	CCC	GTC	TCT	GTG	AGC	CCT	GCC		1138
His	Glu	Pro	Thr	Ile	Ser	Pro	Leu	Thr	Pro	Val	Ser	Val	Ser	Pro	Ala		
						310			315			320					

AAC AGA TCT TCA GTC CAC CCT GCC CCA CCC TTA CAT GAA TCC ATG GCC 1186
Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser Met Ala
325 330 335
CTA GAG CAC TTC TAAGCAGAGA TTATTTGTGA TCCCCATCCAT TCCCCAATAA 1238
Leu Glu His Phe
340
AGCAAGGCTT GTCCGACAAA 1258